

# FIG. 1A

Input file Fbh56919FL2.seq  
Sequence length 3003

TTCCGGCACCAGGCTGCTGCGGGGGGACTCTTTCTGAGGTTACTGTGGAGCACCCAAAGTCTGTCAAGCTCTGGCCCGTGC

AAACAGGCACCCAGAGAACAGACCTTGCTTATTACCCACAGCCCTGGGACTGTCTTCTCCAGAGTCTCCATCAGCTT

TGCTAATCGACTGATTGGAAATAATTCTCAAAACACCAAGTCAAGGATACAGGCAGCGGCTCCCTGTTGTAT

GGACATTCTGCACCCGAACTGATAGCTGAGTCCCTGAAGTTTATGTTATGAACAGAGAAGAACTTTCATCCCGACACAT

M D E S A L T L G T I D V 13  
GATTGGGAATTACACTTTGTGAC ATG GAT GAA TCT GCA CTG ACC CTT GGT ACA ATA GAT GTT 39

S Y L P H S S E Y S V G R C K H T S E E 33  
TCT TAT CTG CCA CAT TCA TCA GAA TAC AGT GTT GGT CGA TGT AAG CAC ACA AGT GAG GAA 99

W G E C G F R P T V F R S A T L K W K E 53  
TGG GGT GAG TGT GGC TTT AGA CCC ACC GTC TTC AGA TCT GCA ACT TTA AAA TGG AAA GAA 159

S L M S R K R P P F V G R C C Y S C T P Q 73  
AGC CTA ATG AGT CGG AAA AGG CCA TTT GTT GGA AGA TGT TGT TAC TCC TGC ACT CCC CAG 219

S W D K F F N P S I P S L G L R N V I Y 93  
AGC TGG GAC AAA TTT TTC AAC CCC AGT ATC CCG TCT TTG GGT TTG CGG AAT GTT ATT TAT 279

I N E T H T R H R G W L A R R L S Y V L 113  
ATC AAT GAA ACT CAC ACA AGA CAC CGC GGA TGG CTT GCA AGA CGC CTT TCT TAC GTT CTT 339

F I Q E R D V H K G M F A T N V T E N V 133  
TTT ATT CAA GAG CGA GAT GTG CAT AAG GGC ATG TTT GCC ACC AAT GTG ACT GAA AAT GTG 399

FIG. 1B

L N S S R V Q E A I A E V A A E L N P D	153
CTG AAC AGC AGT AGA GTA CAA GAG GCA ATT GCA GAA GTG GCT GCT GAA TTA AAC CCT GAT	459
G S A Q Q CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT	173
GGT TCT GCC CAG CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT	519
L Q E M V A T V S P A M I R L T G W V L	193
CTT CAA GAA ATG GTT GCC ACT GTC TCA CCG GCA ATG ATC AGA CTG ACT GGG TGG GTG CTG	579
L K L F N S F F W N I Q I H K G Q L E M	213
CTA AAA CTG TTC AAC AGC TTC TTT TGG AAC ATT CAA ATT CAC AAA GGT CAA CTT GAG ATG	639
V K A A T E T N L P L L F L P V H R S H	233
GTT AAA GCT GCA ACT GAG ACG AAT TTG CCG CTT CTG TTT CTA CCA GTT CAT AGA TCC CAT	699
I D Y L L L L T F I I L F C H N I K A P Y I	253
ATT GAC TAT CTG CTG CTC ACT TTC ATT CTC TTC TGC CAT AAC ATC AAA GCA CCA TAC ATT	759
A S G N N L N I P I F S T L I H K L G G	273
GCT TCA GGC AAT AAT CTC AAC ATC CCA ATC TTC AGT ACC TTG ATC CAT AAG CTT GGG GGC	819
F F I R R R L D E T P D G R K D V L Y R	293
TTC TTC ATA CGA CGA AGG CTC GAT GAA ACA CCA GAT GGA CGG AAA GAT GTT CTC TAT AGA	879
A L L H G H I V E L L R Q Q Q F L E I F	313
GCT TTG CTC CAT GGG CAT ATA GTT GAA TTA CTT CGA CAG CAG CAA TTC TTG GAG ATC TTC	939
L E G T R S R S G K T S C A R A G L L S	333
CTG GAA GGC ACA CGT TCT AGG AGT GGA AAA ACC TCT TGT GCT CGG GCA GGA CTT TTG TCA	999

## FIG. 1C

V V V D T L S T N V I P D I L I I P V G 353  
 GTT GTG GTA GAT ACT CTG TCT ACC AAT GTC ATC CCA GAC ATC TTG ATA ATA CCT GTT GGA 1059  
  
 I S Y D R I I E G H Y N G E Q L G K P K 373  
 ATC TCC TAT GAT CGC ATT ATC GAA GGT CAC TAC AAT GGT GAA CAA CTG GGC AAA CCT AAG 1119  
  
 K N E S L W S V A R G V I R M L R K N Y 393  
 AAG AAT GAG AGC CTG TGG AGT GTA GCA AGA GGT GTT ATT AGA ATG TTA CGA AAA AAC TAT 1179  
  
 G C V R V D F A Q P F S L K E Y L E S Q 413  
 GGT TGT GTC CGA GTG GAT TTT GCA CAG CCA TTT TCC TTA AAG GAA TAT TTA GAA AGC CAA 1239  
  
 S Q K P V S A L L S L E Q A L L P A I L 433  
 AGT CAG AAA CCG GTG TCT GCT CTA CTT TCC CTG GAG CAA GCG TTG TTA CCA GCT ATA CTT 1299  
  
 P S R P S D A A D E G R D T S I N E S R 453  
 CCT TCA AGA CCC AGT GAT GCT GCT GAT GAA GGT AGA GAC AC G TCC ATT AAT GAG TCC AGA 1359  
  
 N A T D E S L R R R L I A N L A E H I L 473  
 AAT GCA ACA GAT GAA TCC CTA CGA AGG AGG TTG ATT GCA AAT CTG GCT GAG CAT ATT CTA 1419  
  
 F T A S K S C A I M S T H I V A C L L L 493  
 TTC ACT GCT AGC AAG TCC TGT GCC ATT ATG TCC ACA CAC ATT GTG GCT TGC CTG CTC CTC 1479  
  
 Y R H R Q G I D L S T L V E D F F V M K 513  
 TAC AGA CAC AGG CAG GGA ATT GAT CTC TCC ACA TTG GTC GAA GAC TTC TTT GTG ATG AAA 1539  
  
 E E V L A R D F D L G F S G N S E D V V 533  
 GAG GAA GTC CTG GCT CGT GAT TTT GAC CTG GGG TTC TCA GGA AAT TCA GAA GAT GTA GTA 1599

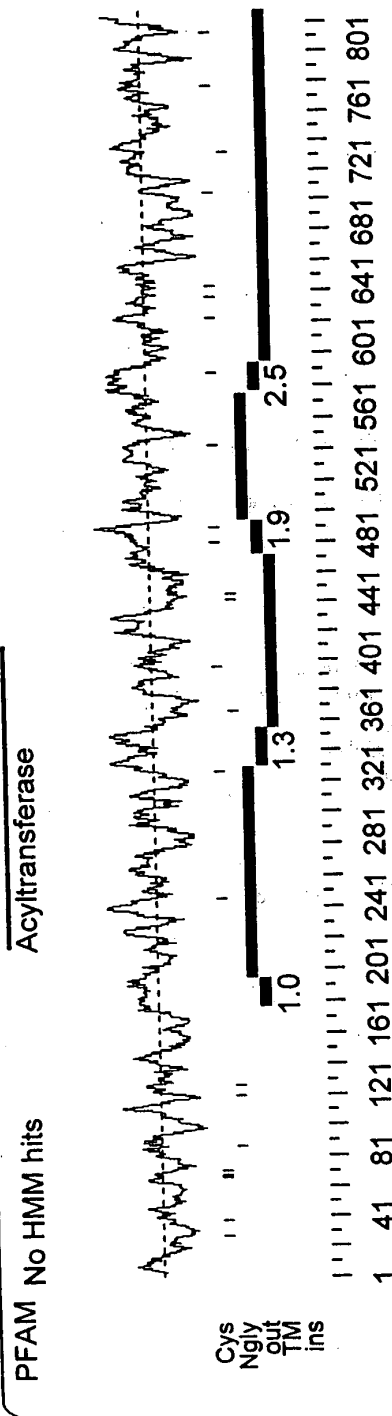
FIG. 1D

M H A I Q L L L G N C V T I T H T S R N D 553  
 ATG CAT GCC ATA CAG CTG CTG GGA AAT TGT GTC ACA ATC ACC CAC ACT AGC AGG AAC GAT 1659  
  
 E F I T P S S T T V P S V F E L N F Y S 573  
 GAG TTT ATC ACC CCC AGC ACA ACT GTC CCA TCA GTC TTC GAA CTC AAC TTC TAC AGC 1719  
  
 N G V L H V F I M E A I I A C S L Y A V 593  
 AAT GGG GTA CTT CAT GTC TTT ATC ATG GAG GCC ATC ATA GCT TGC AGC CTT TAT GCA GTT 1779  
  
 L N K R G L G G P T S T P P N L I S Q E 613  
 CTG AAC AAG AGG GGA CTG GGG GGT CCC ACT AGC ACC CCA CCT AAC CTG ATC AGC CAG GAG 1839  
  
 Q L V R K A A S L C Y L L S N E G T I S 633  
 CAG CTG GTG CGG AAG GCG GCC AGC CTG TGC TGC TAC CTT CTC TCC AAT GAA GGC ACC ATC TCA 1899  
  
 L P C Q T F Y Q V C H E T V G K F I Q Y 653  
 CTG CCT TGC CAG ACA TTT TAC CAA GTC TGC TGC CAT GAA ACA GTA GGA AAG TTT ATC CAG TAT 1959  
  
 G I L T V A E H D D Q E D I S P S L A E 673  
 GGC ATT CTT ACA GTG GCA GAG CAC GAT GAT GAC CAG CAG GAA GAT ATC AGT CCT AGT CTT GCT GAG 2019  
  
 Q Q W D K K L P E P L S W R S D E D E 693  
 CAG CAG TGG GAC AAG AAG CTT CCA GAA CCT TTG TCT TGG AGA AGT GAT GAA GAA GAT GAA 2079  
  
 D S D F G E E Q R D C Y L K V S Q S K E 713  
 GAC AGT GAC TTT GGG GAG GAA CAG CGA GAT TGC TAC CTG AAG GTG AGC CAA TCC AAG GAG 2139  
  
 H Q Q F I T F L Q R L L G P L L E A Y S 733  
 CAC CAG CAG TTT ATC ACC TTC TTA CAG AGA CTC CTT GGG CCT TTG CTG GAG GCC TAC AGC 2199

## FIG. 1E

S A A I F V H N F S G P V P E P E Y L Q 753  
 TCT GCT GCC ATC TTT GTT CAC AAC TTC AGT GGT CCT GTT CCA GAA CCT GAG TAT CTG CAA 2259  
  
 K L H K Y L I T R T E R N V A V Y A E S 773  
 AAG TTG CAC AAA TAC CTA ATA ACC AGA ACA GAA AAT GTT GCA GTA TAT GCT GAG AGT 2319  
  
 A T Y C L L V K N A V K M F K D I G V F K 793  
 GCC ACA TAT TGT CTT GTG AAG AAT GCT GTG AAA ATG TTT AAG GAT ATT GGG GTT TTC AAG 2379  
  
 E T K Q K R V S V L E L S S T F L P Q C 813  
 GAG ACC AAA CAA AAG AGA GTG TCT GTT TTA GAA CTG AGC AGC ACT TTT CTA CCT CAA TGC 2439  
  
 N R Q K L L E Y I L S F V V L \* 829  
 AAC CGA CAA AAA CTT CTA GAA TAT ATT CTG AGT TTT GTG GTG CTG TAG 2487  
  
 GTAAAGTGTGGCAGTGGCAATGAAGTCAATGAGATGAGTTCTCTGTAGGTACCAAGCTTCTGGCTCAAGAGTTTGA  
 AGGTGCCCTTCGACGGGTGAGGCCCTGTNCCGAAGTGATCTCCTGGAAGACAAGTGCCCTTCTNCCCTCCATGGATC  
 TGAGATCTTCCCAGCTTT

FIG. 2



>56919  
MDESALTGLTIDVSYLPHSSEYSVGRCKHTSEEWGEGCFPTVFRSATLKWKESLMSRKR  
PFVGRCCYCTPQSWDKFFNPSPISLGLRNVIYNETHRHRGWLARRLSYVLFQERDV  
HKGMFATNVTENVLSSRVQEAIAEVAELNPDGSAQQQSKAVNKKKAKRILQEMVAT  
VSPAMIRLTGWVLLKLFNSFFWNIQHKGQLEMVKAATETNPLLLFPVHRSHIDYLLLT  
FILFCHNIKAPYIASGNNLNIPFSTLIHKLGFFIRRRIDETPDGRKDVLYRALLHGH  
VELLRQQQFLEIFLEGTRSRSGKTSARAGLLSVVDTLSTNVIPDILIPVGISYDRII  
EGHYNGEQLGPKKNESLWSVARGVIRMLRKNYGCVRVDFAPFSLKEYLESQSQKPVSA  
LLSLEQALLPAILPSRPDADEGRDTSINESRNATDESLRRRLIANLAEHILFTASKSC  
AIMSTHIVACLLLYRHRQIDLSTLVEDEFFVMKEEVLARDFDLGFSGNSEDDVVMHAIQLL  
GNCVTITHTSRNDEFFITPSTTVPSVFELNFYSNGVLHVFIEMAIACSLYAVLNKRGGLG  
GPTSTPPNLI SQEQLVRKAASLCYLLSNEGTSILPCQTFYQVCHETVKGFIQYGILTVAE  
HDDQEDISPSLAEQQWKKLPEPLSWRSDEDEDSDFGEEQRDCYLKVSQSKEHQQTFF  
LQRLGLPLEAYSSAAIFVHNFSGPVPEPEYLQKLHKYLIITRTERNAVAVYAESATYCLVK  
NAVKMFKDIGVFKETKQKRVSVLELSSTFLPQCNRQKLLLEYILSFVVL

# FIG. 3A

## Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM  
 hmmpfam - search a single seq against HMM database  
 HMMER 2.1.1 (Dec 1998)  
 Copyright (C) 1992-1998 Washington University School of Medicine  
 HMMER is freely distributed under the GNU General Public License (GPL).  
 -----  
 HMM file: /prod/ddm/seqanal/PFAM/pfam6.4/Pfam  
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.21255.seq  
 -----

### Query: 56919

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	-----
Acyltransferase	Acyltransferase	126.1	6.4e-34	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Acyltransferase	1/1	215	412 ..	1	195 []	126.1	6.4e-34

## FIG. 3B

Alignments of top-scoring domains:

**Acyltransferase:** domain 1 of 1, from 215 to 412: score 126.1, E = 6.4e-34

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*->lenlpkkgpaivvsNHRsYdIlvlsaalprrgpwlrvrlvfiakke
+ +++++ p ++ + HRS++D+l+l ++l++++ ++ +ia ++
56919 215 KAATETNLP LLFLPVHRSHIDYLLLTFFILFCHN----IKAPYIASGN 257

llkvPllfGwlmrlagaifidRnnra.....kdalaaadelvrvlellrk
+l++P+ f++l+ ++g +fi+R+ +++++++kd l++a+ + + tellr+
56919 258 NLNIPI-FSTLIHKLGGFFIRRLDEtpdgrKDVLyrALLHGHIVELLRQ 306

grsvliFPEGTRsrsgellppfKkGia.....afrlAlkagvpivPvviv
+ + iF EGTRsrsg++ + ++G+++ + + ++ ++ i+Pv+i
56919 307 QQFLEIFLEGTRSRSGKTSC-ARAGLLsvvvdTLSTNVIPDILIIIPVGI- 354

sgteelepknagkllLrlarkkpgvtvrvlppld..pedikelaelr
s++ ++e +++ + +++k+++++ v +++ ++++ +++++ +
56919 355 SYDRIIEGHYNGEQ--LGKPKKNESLWSVARGVIRMLrKNYGCVRVDFQAQ 402

dilvqaleel<-*
+ ++++ e+
56919 403 PPSLKEYLES 412

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## FIG. 4A

ProDom Matches ProdomId	Start	End	Description	Score
View Prodom PD347660	1	55	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	250
View Prodom PD087501	51	158	p2001.1 (1) // AIP2-DLD1	77
View Prodom PD353751	56	152	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	500
View Prodom PD037846	128	259	p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR MITOCHONDRION	258
View Prodom PD042466	259	590	p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE MITOCHONDRION	413
View Prodom PD025192	462	649	p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION	

# FIG. 4B

458

View Prodom PD042027 465 673 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE  
GLYCEROL-3-PHOSPHATE MEMBRANE  
PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT

80

View Prodom PD042760 650 828 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE  
PHOSPHOLIPID BIOSYNTHESIS PRECURSOR  
TRANSMEMBRANE GLYCEROL-3-PHOSPHATE  
GPAT MITOCHONDRION MITOCHONDRIAL

799

View Prodom PD042760

>PD042760 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS  
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION  
MITOCHONDRIAL  
Length = 179

Score = 799 (286.3 bits), Expect = 1.2e-79, P = 1.2e-79  
Identities = 155/179 (86%), Positives = 161/179 (89%)

Query: 650 FIQYGILTVAEHDDQEDISPLAEQQWDKKLPEPLSWRXXXXXXXXXXXXXQDCCYLKVS 709  
FIQYGILTVAE DDQED+SP LAEQQW+KKLPEPL+WR QDCCYLKVS

Sbjct: 1 FIQYGILTVAEQDDQEDVSPGLAEQQWNKKLPEPLNWRSDDEEDSDFGEEQDCCYLKVS 60

Query: 710 QSKEHQQFITFLQRLLGPLLEAYSSAAIFVHNFGSPVPEPEYLQKLHKYLITRTERNVAV 769  
Q+KEHQQFITFLQRLLGPLLEAYSSAAIFVHNFGSPVPEPEYLQKLHKYLITRTERNVAV

Sbjct: 61 QAKEHQQFITFLQRLLGPLLEAYSSAAIFVHNFGSPVPEPEYLQKLHKYLITRTERNVAV 120

Query: 770 YAESATYCLVKNVAVKMFKDGVFKETKQKRVSVLELSSTFLPQCNRQKLLEYILSFVVL 828  
YAESATYCLVKNVAVKMFKDGVFKETKQKRVSVLELS+TFLPQCNRQKLLEYILSFVVL

Sbjct: 121 YAESATYCLVKNVAVKMFKDGVFKETKQKRVSVLELSSTFLPQCNRQKLLEYILSFVVL 179

## FIG. 4C

View Prodom PD353751

>PD353751 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS  
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION  
 MITOCHONDRION

Length = 97

Score = 500 (181.1 bits), Expect = 2.1e-47, P = 2.1e-47  
 Identities = 90/97 (92%), Positives = 97/97 (100%)

Query: 56 MSKRPFVGRCCYSCCTPQSWDKFFNPSISLGLRNVIYINETHTRHGWLARRLSYVLEI 115  
 MSKRPFVGRCCYSCCTPQSW++FFNPSISLGLRNVIYINETHTRHGWLARRLSY+LE+  
 Sbjct: 1 MSKRPFVGRCCYSCCTPQSWERFFNPSISLGLRNVIYINETHTRHGWLARRLSYILFV 60

Query: 116 QERDVHKGMFATNVNVLNSSRVQEAIAEVAEALNP 152  
 QERDVHKGMFAT++T+NVLNSSRVQEAIAEVAEALNP  
 Sbjct: 61 QERDVHKGMFATSITDNVLNSSRVQEAIAEVAEALNP 97

View Prodom PD025192

>PD025192 p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRION  
 BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT  
 MITOCHONDRION

Length = 194

Score = 458 (166.3 bits), Expect = 8.7e-43, P = 8.7e-43  
 Identities = 95/192 (49%), Positives = 126/192 (65%)

Query: 462 RRLIANLAEHILFTASKSCAIMSTHIVACLLLYRHRQGDILSTLVEDEFFVMKEEVLARDF 521  
 R LI ++ EH++F S C+IMSTH+VACLLL R R G+ STL ED + E++LA  
 Sbjct: 3 RNLIRSIGEHVVFDCSMMCSIMSTHVACLLLTRWRNGVHRSTLEEDCDWLCEKILAEAG 62

## FIG. 4D

Query: 522 DL-GFSGNS---EDVVMHAIQLLNCVCTITHTSRNDEFFITPSTVPSVFELNFYNGVL 577  
 D+ GFSG S +V +A +LLG+CVT+T RNDEF+I+P +VPS EL +YSN V+

Sbjct: 63 DIVFGSKSTKGSQIVKYACELLGSCVTVDDEDRNDEFYISPKNVPSFIELAYYSNSVI 122

Query: 578 HVFIMEAIIACSLYAVLNKRGGLGPTSTPPNLISQQLVRKAASLCYLLSNEGTLISLPCQ 637  
 F +++IIAC++Y++ NK GG NLISQQLV A SLC L E PCQ

Sbjct: 123 CHFALKSIIACTIYSLPNKTKNGGEAGGLNLISQQLVEDALSCLDWLQYEFMFCRPCQ 182

Query: 638 TFYQVCHETVGK 649  
 T ++CH T+GK

Sbjct: 183 TLRELCHNTLGK 194

View Prodom PD042466

>PD042466 p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE  
 BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE  
 MITOCHONDRION

Length = 299

Score = 413 (150.4 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42  
 Identities = 79/152 (51%), Positives = 108/152 (71%)

Query: 259 LNIPIFSTLIHKLGFFIRRLDETDPGRKDVLYRALLHGHIVELLRQQQFLEIFLEGTR 318  
 L++PI +L+ + G FFIRR D TP+G+ D LYRA+ H ++ +L+ + +E F+EGTR

Sbjct: 2 LSPIMGSLLRRTGAFFIRSFDPTEPGKGDQLYRAVFEHYVAQLISKGYNIEFFIEGTR 61

Query: 319 SRSGKTSCARAGLLSVVVDLTSTNVIPDILIPVGISYDRIIEGH-YNGEQLGKPKKNES 377  
 SR+GK + GLLS+VV+ +PDIL++PV ISYDRIIEG+ Y E G PKK ES

Sbjct: 62 SRTGKMLPPKGTGLLSMVVEAFLRGSVPDILLVPVSIYDRIIEGNTYAHELRGAPKKES 121

## FIG. 4E

Query: 378 LMSVARGVIRMLRKNYGCVRVDFEAQPFSLKEY 409  
 LW + RGV +ML++NYG V VDF +P SL+EY  
 Sbjct: 122 LWQLFRGVRKMLKRNYGQVYVDFEGEPISLREY 153

Score = 64 (27.6 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42  
 Identities = 30/143 (20%), Positives = 59/143 (41%)

Query: 453 RNATDESILRRRLIANLAEHILFTASKSCAIMSTHIVACLLLYRHRQGIDLSTL---VEDF 509  
 RN + + +R + ++ + + ++ + +T +V+ LLL + L L ++D  
 Sbjct: 160 RNTYNCAPKRLALQKMSFEVAVWRILQATPVTATGLVSALLLTTRGTALTLDQLHHTLQDS 219

Query: 510 FVMKEEVLARDFDLGFGNSEDDVMHAIQLL--GNCVTITHTSRNDEFFITPSTTVPSVF 567  
 E + S + V A L G+ VT + R ++I P + F  
 Sbjct: 220 LDYLERKQSPVSTALRLRSREGVRAAADALSNGHPVTRVDSGREPVWYIAPDDEHAAAF 279

Query: 568 ELNFYSNGVLHVFIEMAIACSL 590  
 Y N V+H F+ +I+ +L  
 Sbjct: 280 ----YRNSVIHAFLETSIVELAL 298

View Prodom PD037846

>PD037846 p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE  
 PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR  
 MITOCHONDRION  
 Length = 345

Score = 258 (95.9 bits), Expect = 3.4e-21, P = 3.4e-21  
 Identities = 56/132 (42%), Positives = 79/132 (59%)

## FIG. 4F

Query: 128 NVTENVLNSSRVQEAIAEVAELNPDGSAQQQXXXXXXXXXXRIQLQEMVATVSPAMIR 187  
 N+ +NVLNS + I + A++ S IL EM T++ MIR  
 Sbjct: 223 NLKKNVLNSEEIHYVIEQ-----EAKESSTSIDKVRREAREILDEMSHTLNMG MIR 273

Query: 188 LTGWVLLKLFNSFFWNIIHKGQLEMVKAATETNLP LLFVPVHRSHIDYLLLTFFILFCHN 247  
 GWVL K+FN F I +++ Q+E +K ATE P+++LP HRSHIDYLL+FIL+ ++  
 Sbjct: 274 FCGWVLSKIFNRIFSGICVNEEQIEKIKRATEGHPVIYLPVHRSHIDYLLLSFILYHYD 333

Query: 248 IKAPYIASGNNL 259  
 IK P+IA+G NL  
 Sbjct: 334 IKVPHIAAGMNL 345

View Prodom PD347660

>PD347660 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS  
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION  
 MITOCHONDRIAL  
 Length = 55

Score = 250 (93.1 bits), Expect = 2.4e-20, P = 2.4e-20  
 Identities = 43/55 (78%), Positives = 53/55 (96%)

Query: 1 MDESALTIGTIDVSYLPHSSEYSVGRCKHTSEEWGECGFRPTVFRSATLKWKESL 55  
 M+ES++T+GTIDVSYLP+SSEYS+GRCKHT+E+W +CGF+PT FRSATLKWKESL  
 Sbjct: 1 MEESVTIGTIDVSYLPNSSEYSGLRCKHTNEDWDCGFKPTFFRSATLKWKESL 55

## FIG. 4G

View Prodom PD042027

>PD042027 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE  
 PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT  
 Length = 345

Score = 80 (33.2 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 31/129 (24%), Positives = 60/129 (46%)

Query: 465 IANLAEHILFTASKCAIMSTHIVACLLLYRHRQIDLSTLVE--DFFVMKEEVLA RFD 522  
 + +LA+ I+ + + A+ ++ A LL ++ + L+E D ++ + D

Sbjct: 32 VNHLAKQIMTHINDAAAVNPMNLCATALLSTRQALGEEQLIEQLDCYLKLLRNVPYSTD 91

Query: 523 LGFSGNS-EDVVMHAIQ--LLGNCVTITHTSRNDEFFITPSTTVPSVFELNFYSNGVLHV 579  
 ++ E ++ HA Q LLG VT+ + D + V + +Y N VLH+

Sbjct: 92 ATLPDHTPERLIEHAEQMNLIG--VTVEKDTLGILRLDRDNAV L-----MTYYRNNVLHL 145

Query: 580 FIMEAIIAC 588  
 F + A++AC

Sbjct: 146 FALPALVAC 154

Score = 62 (26.9 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 22/105 (20%), Positives = 48/105 (45%)

Query: 569 LNFYSNGVLHV FIMEAIIACSLYAVLNKRG LGGPTSTPPNLISQQLVRKAASLCYLLSN 628  
 + +Y N VLH+F + A++AC N+R IS++ L+R +L L

Sbjct: 135 MTYYRNNVLHLFALPALVACCFKN--NRR-----ISR DALLRFVRALYPFLQA 180

Query: 629 EGTISLPCQTFYQVCHETVKGFIQYGILTVAEHDDQEDISPSLAE 673  
 E + + + +F++ G+L A + + + ++ + ++

Sbjct: 181 ELFLRWNEDELNDHIDQWINEFVRQGLLSAGNQEDDTLTRNTSQ 225

## FIG. 4H

View Prodom PD087501

>PD087501 p2001.1 (1) // AIP2-DLD1  
 Length = 170

Score = 77 (32.2 bits), Expect = 5.1, P = 0.994  
 Identities = 31/114 (27%), Positives = 44/114 (38%)

Query: 51 WKES--LMSRKRPFVGRCCYCTPQSWDKFFNPSPISGLRNVIYINETHTRHGWLARR 108  
 W ES L+ RK F RCC P K + L N +H W  
 Sbjct: 12 WNESEVLVDRKSKFQARCC----PLQNQKDIPSILQELTQNNKSVSKASHMHMYAWRTAE 67

Query: 109 LSYVLFIQERDVHKGMFATNVTENVLNSSR---VQ-EAIAEVAELNPDGSAQQ 158  
 +S L +Q+ KG A + +N SR VQ + I + A+ G+ Q+  
 Sbjct: 68 VSNNLHLQQEQKKGNKANKSNNSHVNKS RNITVQPKNIEQGCADCCEAGAGQR 121



## FIG. 5A

	10	20	30	40	
1	MDESALT LGTIDVSYLP HSSEYSVGRCKHTSEEWGECGFR				56919.pro
1	MEESSVT VGTIDVSYLPSSSEYSLGRCKHTSEDWVDCGFK				MouseGPAT.PRO
1	MEESSVTIGTIDVSYLPNSSEYSLGRCKHTNEDWVDCGFK				RatGPAT.PRO
	50	60	70	80	
41	PTVFRSATL KWKESLMSRK RPFVGRCCYSCTPQSWDKFFN				56919.pro
41	PTFFRSATL KWKESLMSRK RPFVGRCCYSCTPQSWERFFN				MouseGPAT.PRO
41	PTFFRSATL KWKESLMSRK RPFVGRCCYSCTPQSWERFFN				RatGPAT.PRO
	90	100	110	120	
81	PSIPSLGLRNVIYINETHTRHRGWLARRLSYVLFQERDV				56919.pro
81	PSIPSLGLRNVIYINETHTRHRGWLARRLSYILFVQERDV				MouseGPAT.PRO
81	PSIPSLGLRNVIYINETHTRHRGWLARRLSYILFVQERDV				RatGPAT.PRO
	130	140	150	160	
121	HKGMFATNV TENVLNSSRVQEAIAEVAELNPDGSAQQQS				56919.pro
121	HKGMFATSV TENVLSSSRVQEAIAEVAELNPDGSAQQQS				MouseGPAT.PRO
121	HKGMFATSITDNVLNSSRVQEAIAEVAELNPDGSAQQQS				RatGPAT.PRO
	170	180	190	200	
161	KAVNKVKKKAKRILQEMVATVSPAMIRLTGWVLLKLFNSF				56919.pro
161	KAIQKVKRKARKILQEMVATVSPGMIRLTGWVLLKLFNSF				MouseGPAT.PRO
161	KAIQKVKRKARKILQEMVATVSPGMIRLTGWVLLKLFNSF				RatGPAT.PRO
	210	220	230	240	
201	FWNIQIHKQLEMVKAATETNLP LLFLPVHRSHIDYLLLT				56919.pro
201	FWNIQIHKQLEMVKAATETNLP LLFLPVHRSHIDYLLLT				MouseGPAT.PRO
201	FWNIQIHKQLEMVKAATETNLP LLFLPVHRSHIDYLLLT				RatGPAT.PRO
	250	260	270	280	
241	FILECHNIKAPYIASGNNLNIPFSTLIHKLGGFFIRRRRL				56919.pro
241	FILECHNIKAPYIASGNNLNIPVSTLIHKLGGFFIRRRRL				MouseGPAT.PRO
241	FILECHNIKAPYIASGNNLNIPFSTLIHKLGGFFIRRRRL				RatGPAT.PRO
	290	300	310	320	
281	DETPDGRKDVLYRALLHGHIVELLRQQQFLEIFLEGTRSR				56919.pro
281	DETPDGRKDILYRALLHGHVVELLRQQQFLEIFLEGTRSR				MouseGPAT.PRO
281	DETPDGRKDILYRALLHGHIVELLRQQQFLEIFLEGTRSR				RatGPAT.PRO
	330	340	350	360	
321	SGKTSCARAGLLSVVVDTLSTNVIPDILIPVGISYDRII				56919.pro
321	SGKTSCARAGVLSVVNTLSSNTIPDILIPVGISYDRII				MouseGPAT.PRO
321	SGKTSCARAGLLSVVVDTLSSNTIPDILIPVGISYDRII				RatGPAT.PRO

## FIG. 5B

	370	380	390	400	
361	EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGCVRVDF				56919.pro
361	EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF				MouseGPAT.PRO
361	EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF				RatGPAT.PRO
	410	420	430	440	
401	AQPFSLKEYLESQSQKPVSAALLSLEQALLPAILPSRPSDA				56919.pro
401	AQPFSLKEYLEGQSQKPVSAPLSLEQALLPAILPSRPNDV				MouseGPAT.PRO
401	AQPFSLKEYLEGQSQKPVSAPLSLEQALLPAILPSRPDAA				RatGPAT.PRO
	450	460	470	480	
441	ADEGRDTSINESRNATDESLRRRLIANLAEHILETASKSC				56919.pro
441	ADEHQDLSINESRNPADEAFRRRLIANLAEHILETASKSC				MouseGPAT.PRO
441	AAEHEDMSINESRNAADEAFRRRLIANLAEHILETASKSC				RatGPAT.PRO
	490	500	510	520	
481	AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD				56919.pro
481	AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD				MouseGPAT.PRO
481	AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEVLARD				RatGPAT.PRO
	530	540	550	560	
521	FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRNDEFFITPS				56919.pro
521	FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS				MouseGPAT.PRO
521	FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS				RatGPAT.PRO
	570	580	590	600	
561	TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVLNKRGLG				56919.pro
561	TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVLNKRCSG				MouseGPAT.PRO
561	TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVQNKRGS				RatGPAT.PRO
	610	620	630	640	
601	GPTSTPPNLISQEQVLRKAASLCYLLSNEGTISLPCQTFY				56919.pro
601	GPTSTPPNLISQEQVLRKAASLCYLLSNEGTISLPCQTFY				MouseGPAT.PRO
601	GPTSTPPNLISQEQVLRKAASLCYLLSNEGTISLPCQTFY				RatGPAT.PRO
	650	660	670	680	
641	QVCHETVGKFIQYGILTVAEHDDQEDISPSLAEQQWDKKL				56919.pro
641	QVCHETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWDKKL				MouseGPAT.PRO
641	QVCQETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWNKKL				RatGPAT.PRO
	690	700	710	720	
681	PEPLSWRSDEEDEDSDFGEEQRDCYLKVSQSKEHQQFITY				56919.pro
681	PE-LNWRSD E EDEDSDFGEEQRDCYLKVSQSKEHQQFITY				MouseGPAT.PRO
681	PEPLNWRSD E EDEDSDFGEEQRDCYLKVSQAKEHQQFITY				RatGPAT.PRO

## FIG. 5C

	730	740	750	760	
721	LQRLLGPLEAYSSAAIFVHNFSGPVPEPEY LQKLHKYLI				56919.pro
721	LQRLLGPLEAYSSAAIFVHNFSGPVPEPEY LQRLHKYLI				MouseGPAT.PRO
721	LQRLLGPLEAYSSAAIFVHTFRGPVPEPEY LQRLHKYLI				RatGPAT.PRO
	770	780	790	800	
761	TRTERNVAVYAESATYCLVKNVAVKMEKDIGVFKETKQKRV				56919.pro
761	TRTERNVAVYAESATYCLVKNVAVKMEKDIGVFKETKQKRV				MouseGPAT.PRO
761	TRTERNVAVYAESATYCLVKNVAVKMEKDIGVFKETKQKRA				RatGPAT.PRO
	810	820			
801	SVLELSSTFLPQCNRQKLLEYILSFVVL				56919.pro
801	SVLELSSTFLPQCNRQKLLEYILSFVVL				MouseGPAT.PRO
801	SVLELSSTFLPQCNRQKLLEYILSFVVL				RatGPAT.PRO

## FIG.6

## Acyltransferase catalytic motif-I

<u>IFLEGTRSR</u>	56919.pro
IFLEGTRSR	MouseGPAT.PRO
IFLEGTRSR	RatGPAT.PRO
YFVEGGRSR	EcoliGPAT.PRO

## Acyltransferase catalytic motif-II

<u>HRSHID</u>	56919.pro
HRSHID	MouseGPAT.PRO
HRSHID	RatGPAT.PRO
HRSHMD	EcoliGPAT.PRO

## Acyltransferase catalytic motif-III

<u>ILIIPV</u>	56919.pro
ILVIPV	MouseGPAT.PRO
ILVIPV	RatGPAT.PRO
ITLIPI	EcoliGPAT.PRO

## Acyltransferase signature motif

<u>GGFFIRR</u>	56919.pro
GGFFIRR	MouseGPAT.PRO
GGFFIRR	RatGPAT.PRO
GAFFIRR	EcoliGPAT.PRO

FIG. 7A

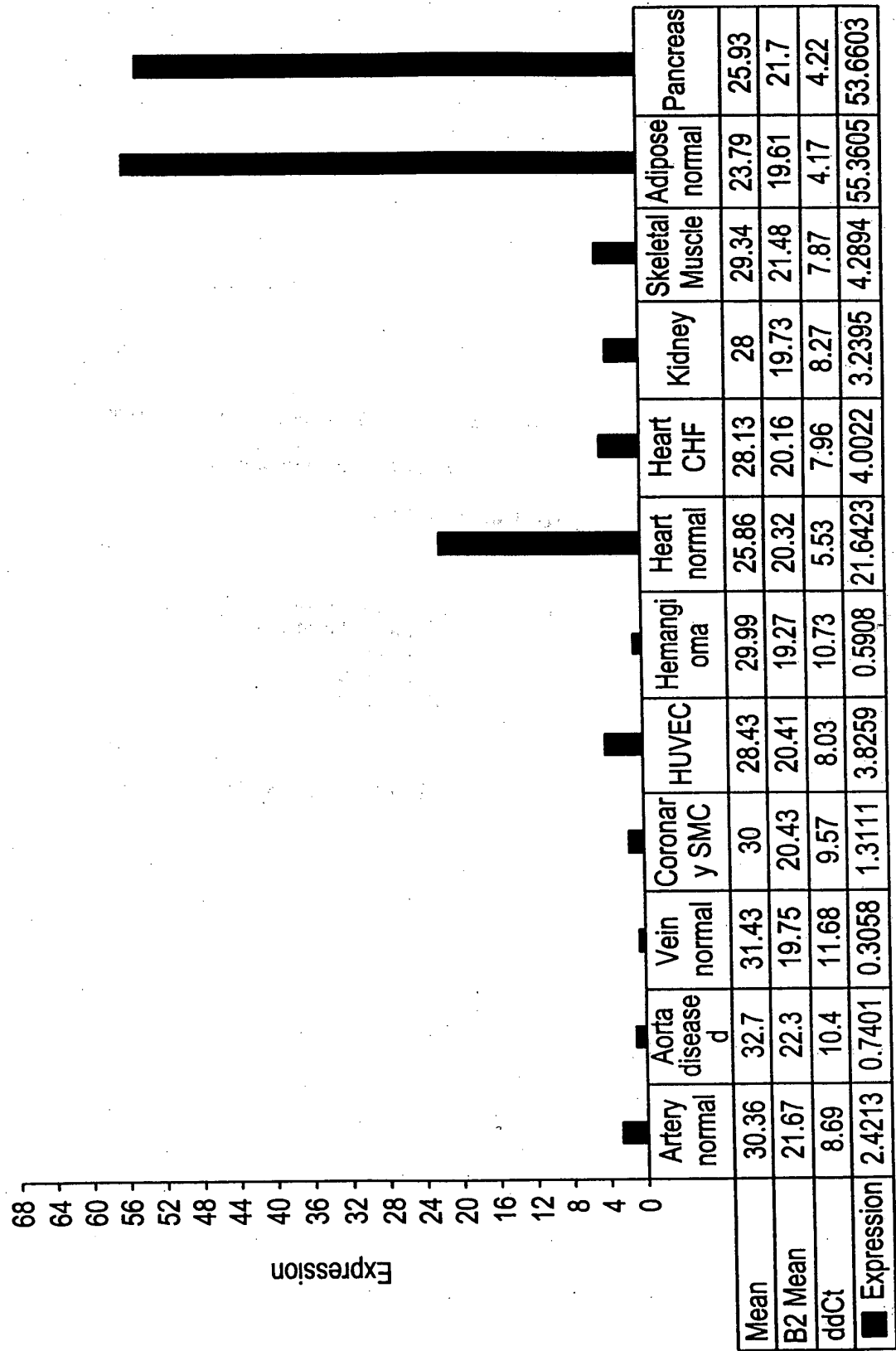


FIG. 7B

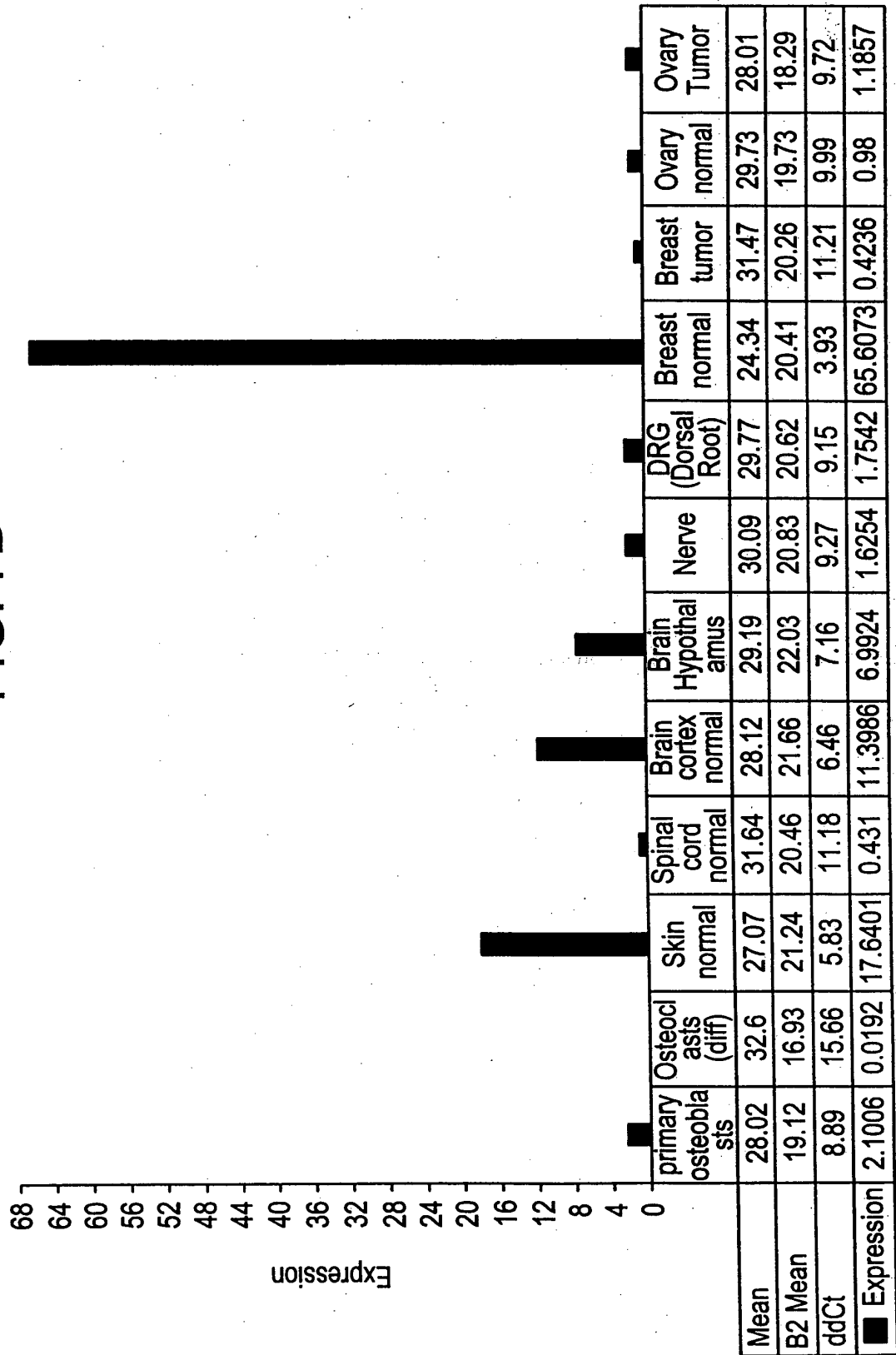


FIG. 7C

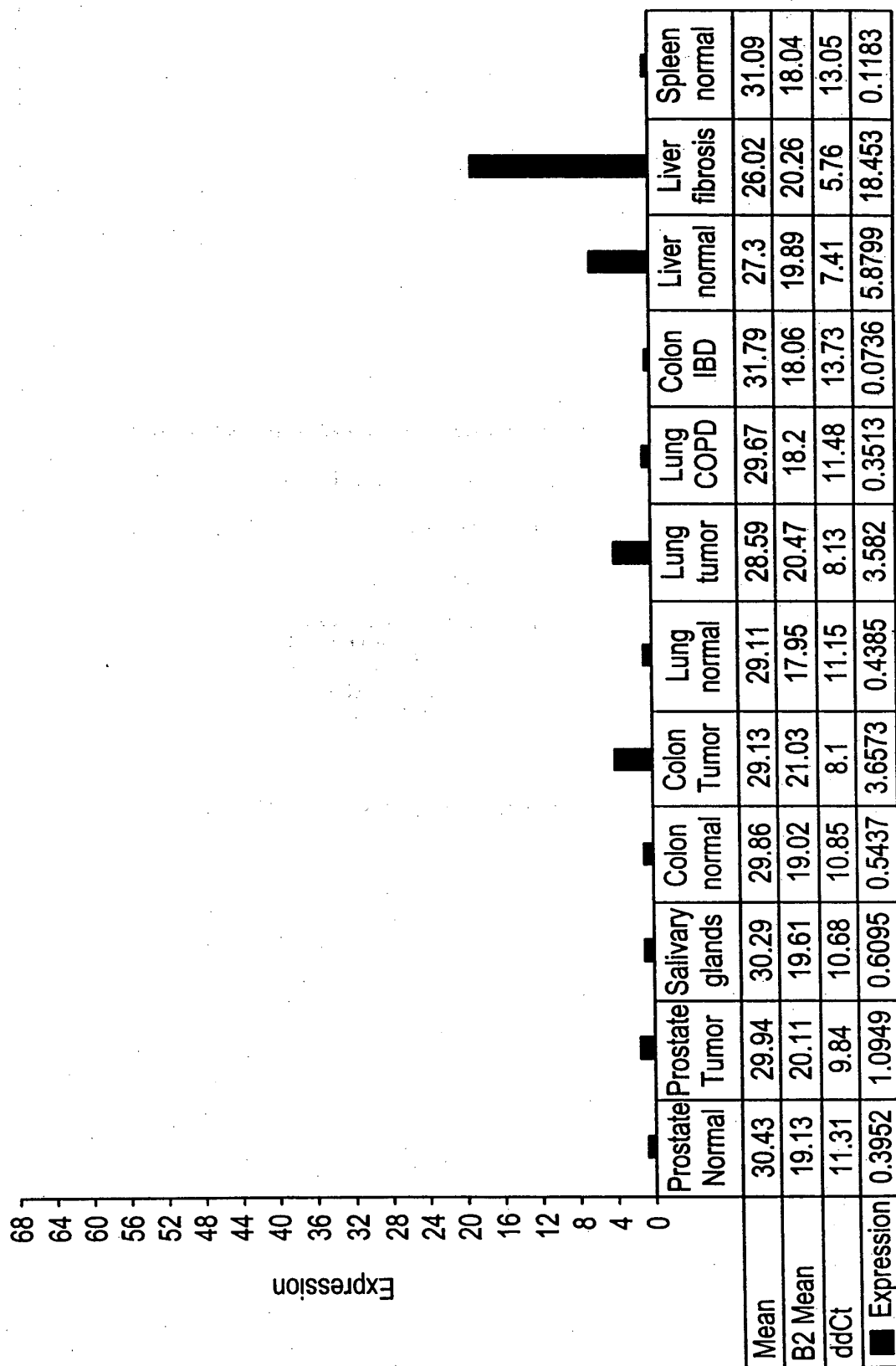


FIG. 7D

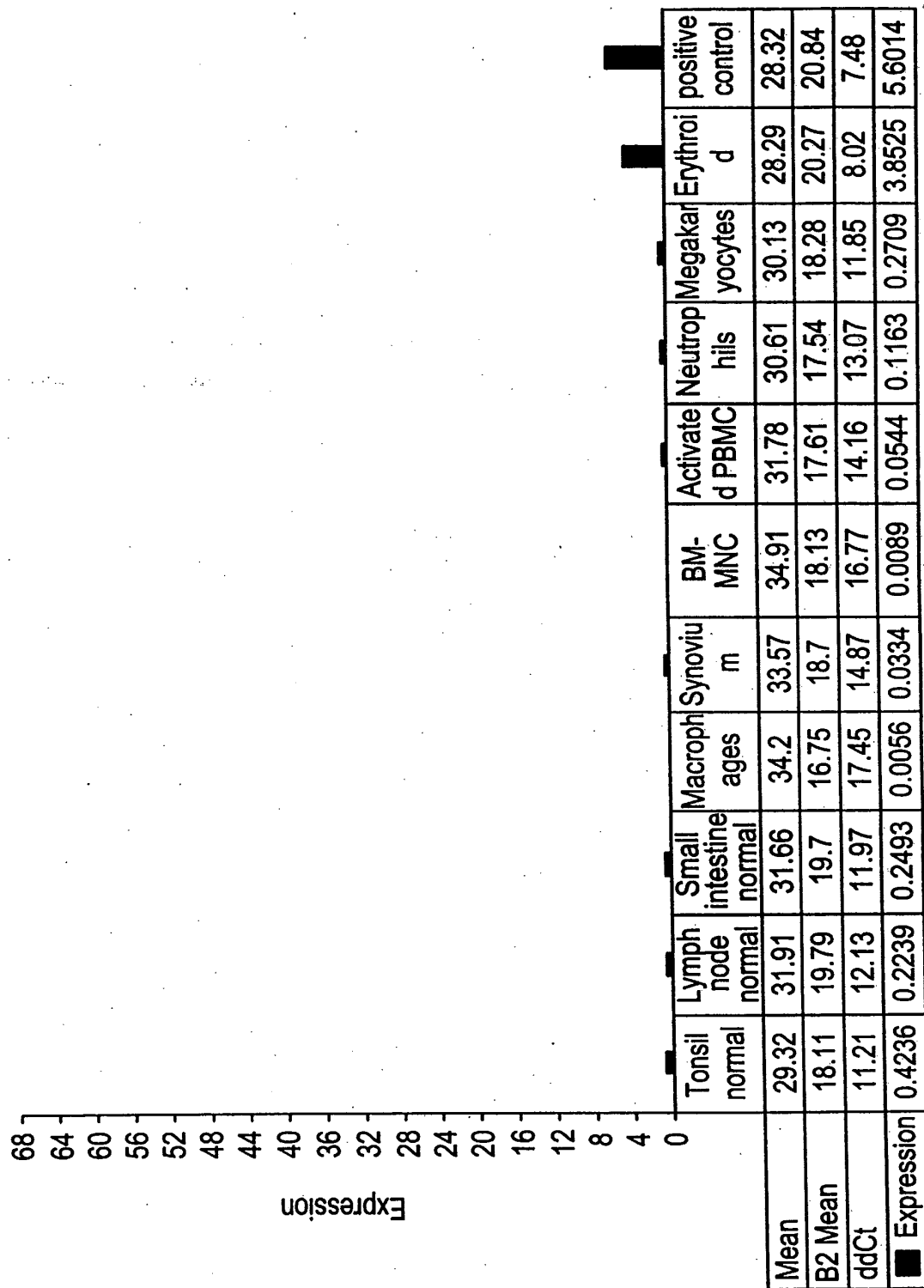




FIG. 8A

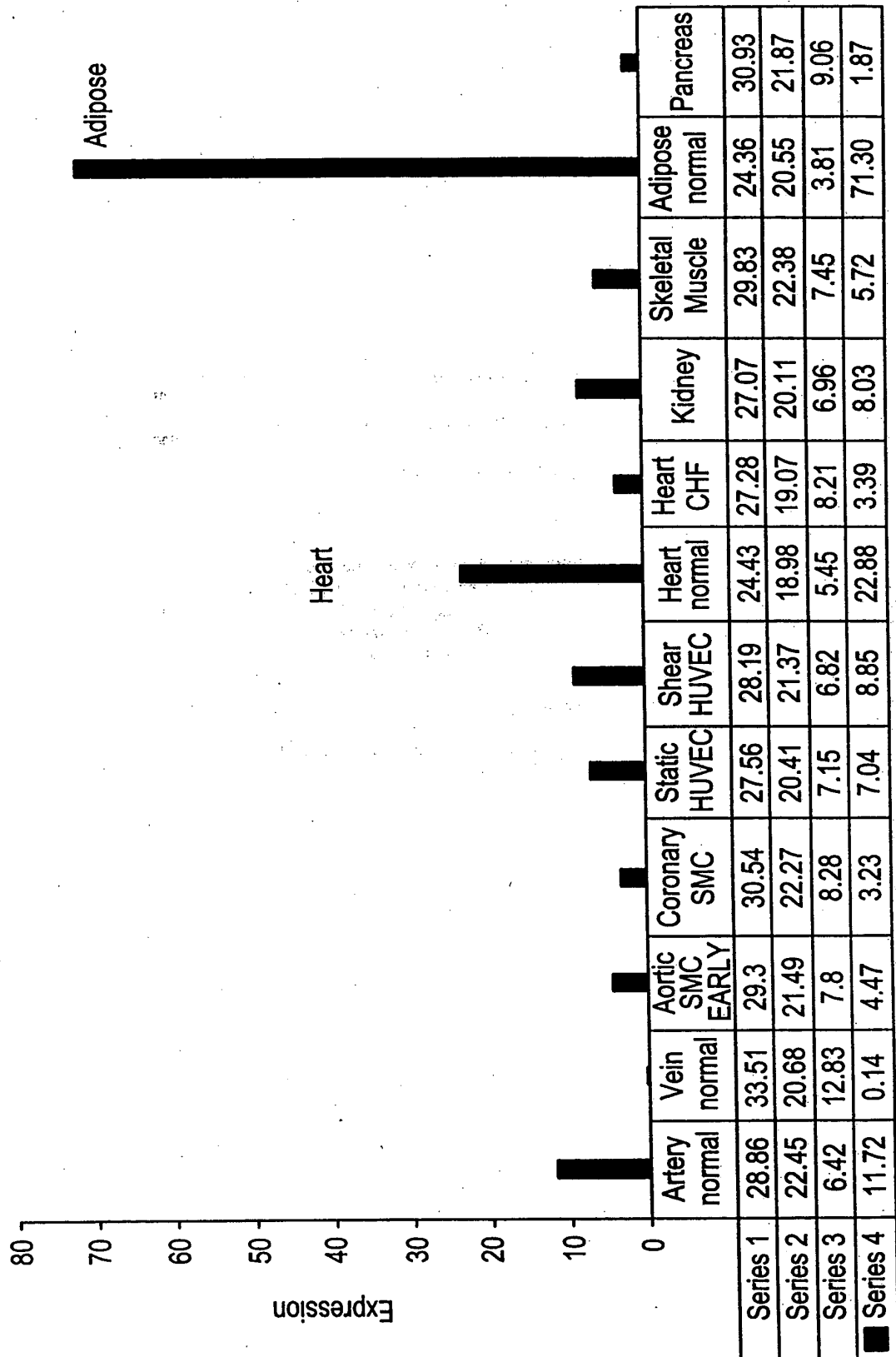


FIG. 8B

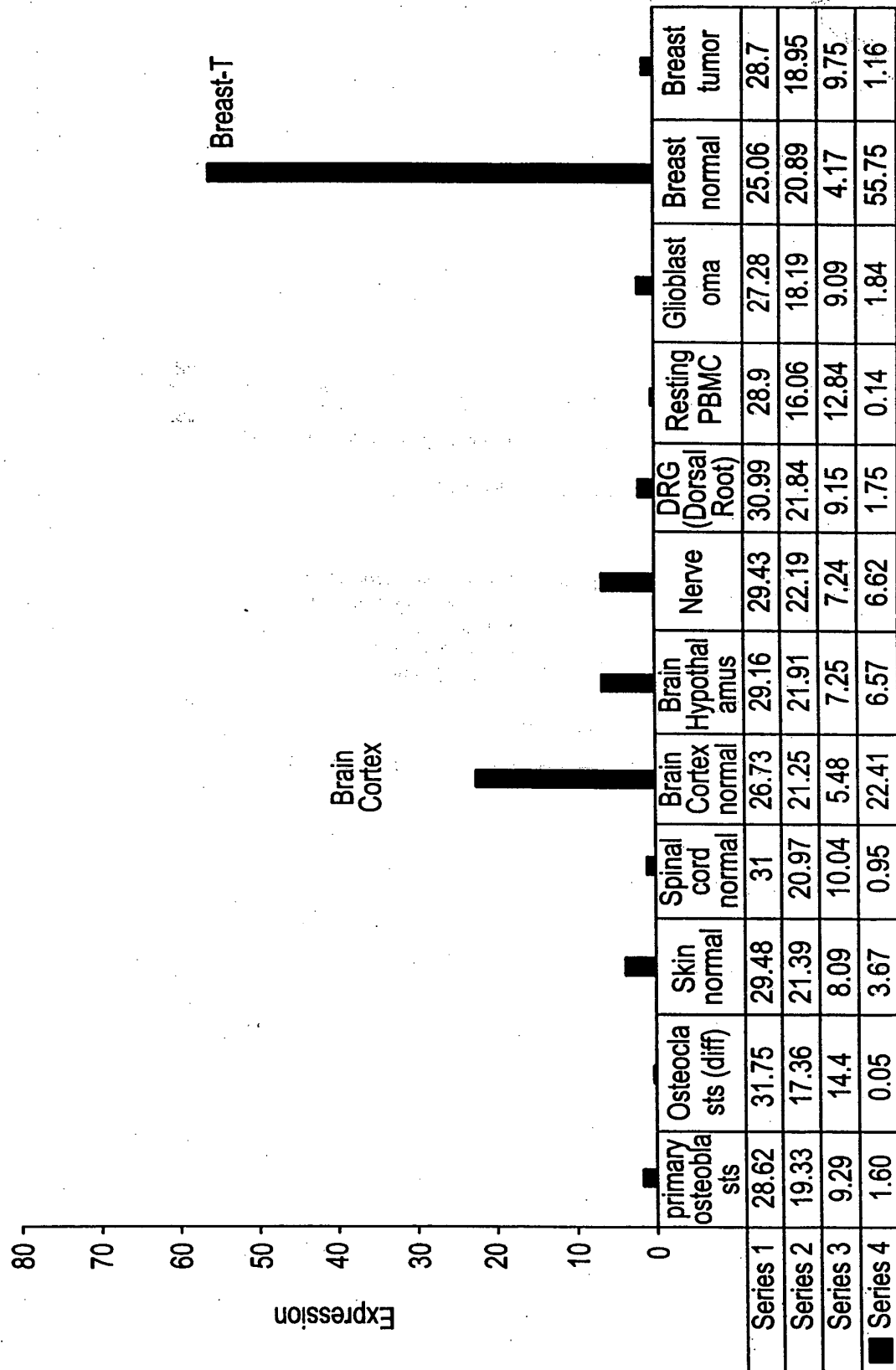


FIG. 8C

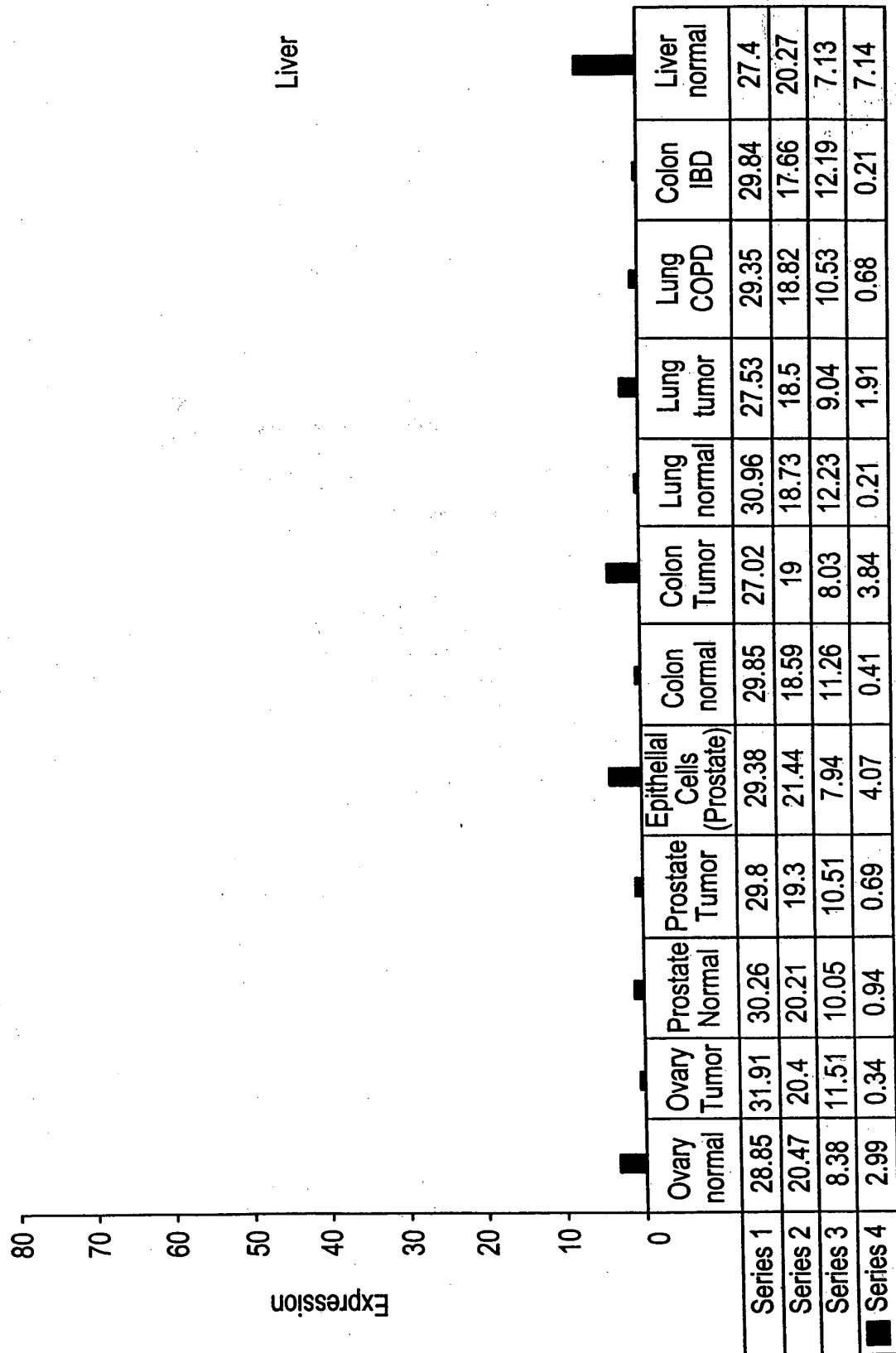


FIG. 8D

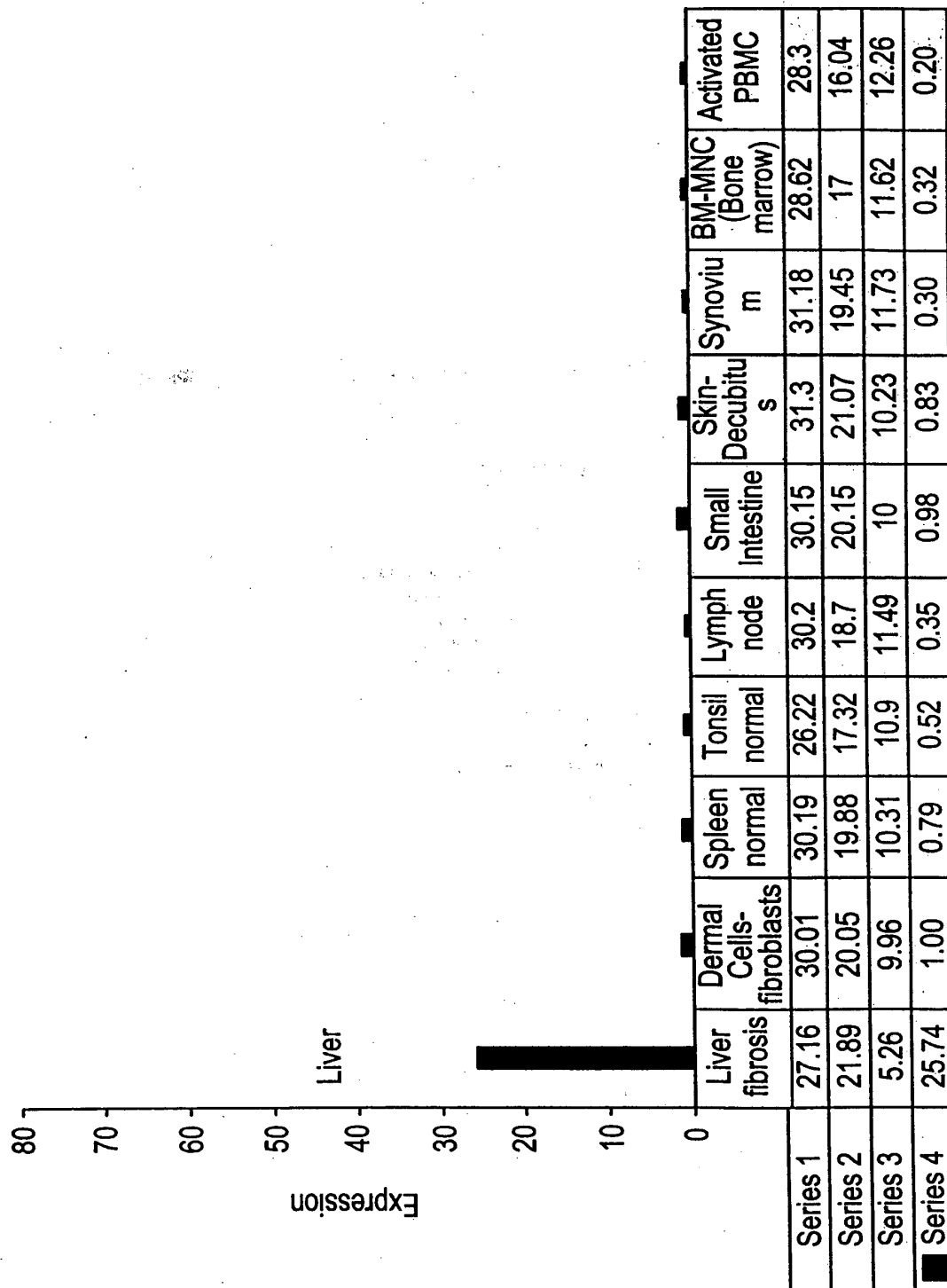


FIG. 9A

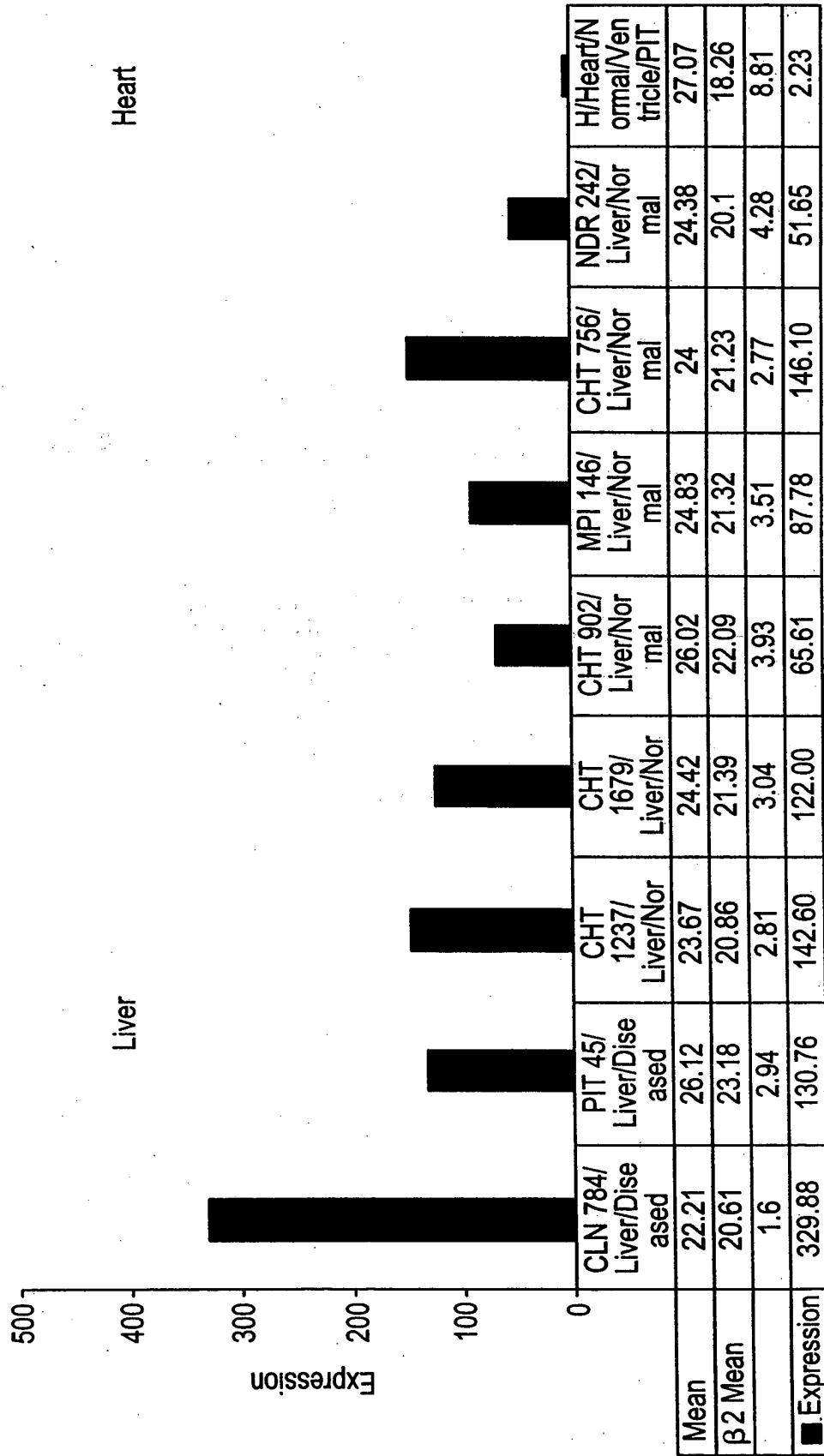


FIG. 9B

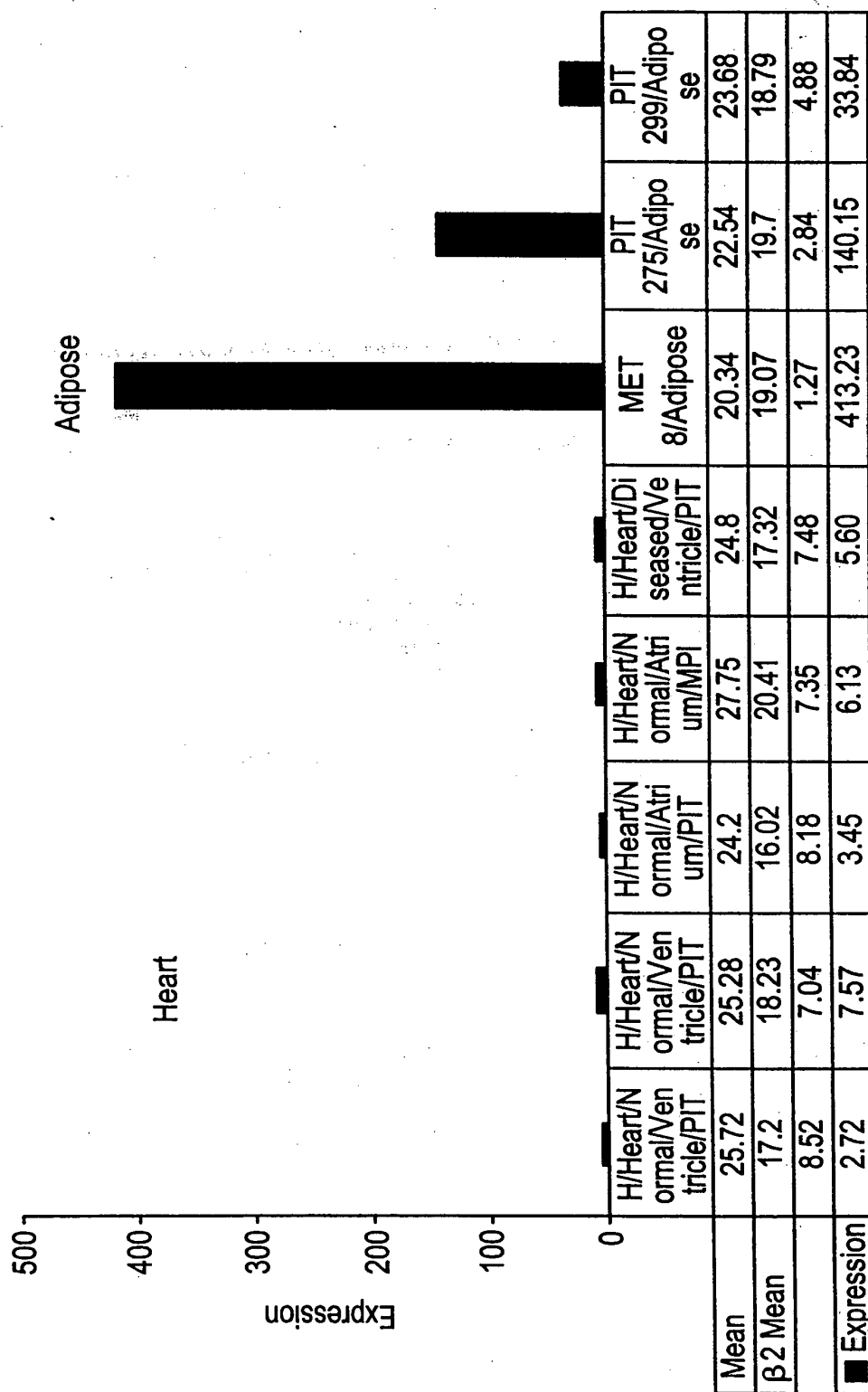


FIG. 10A

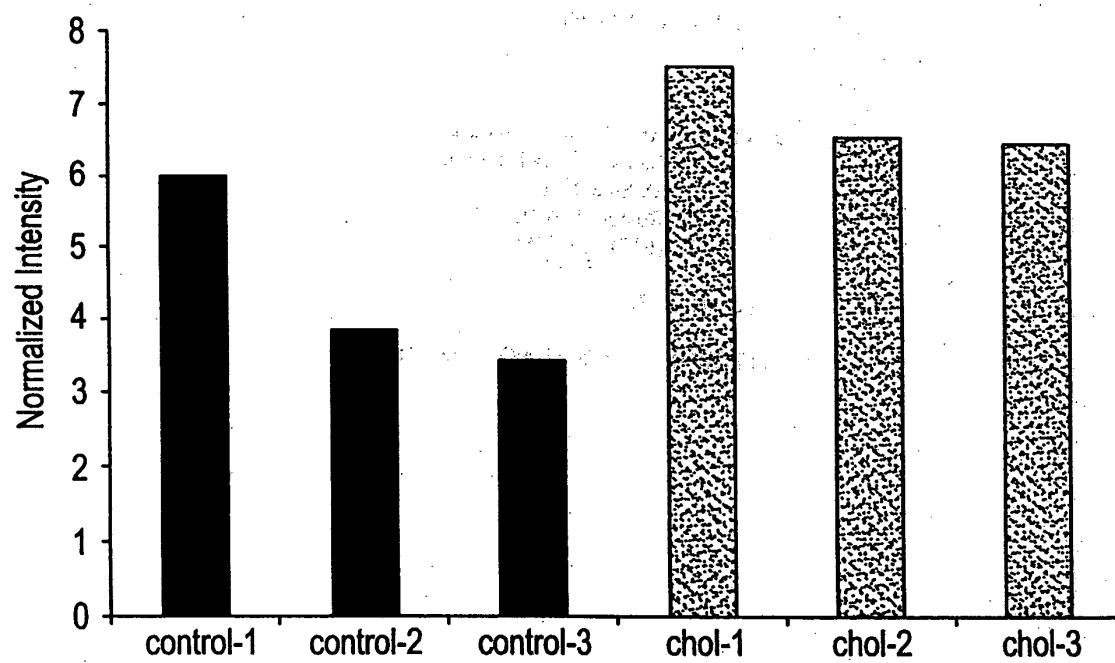


FIG. 10B

